**Amendments to the Specification:**

Please replace the paragraph at page 11, lines 1-19, with the following:

The consensus sequence for the ATP-binding motif is located at positions 617-627. When compared with other kinases, the ATP binding domain is ~~with~~ 176 amino acids (including the additional 37 amino acids) further from the transmembrane domain than any other tyrosine kinase. The additional 37 amino acids are located in the long and proline/glycine-rich juxtamembrane region and contain an NPAY sequence (SEQ ID NO:5) (where A can be exchanged for any amino acid), which is found in cytoplasmic domains of several cell surface proteins, including RTKs of the EGF and insulin receptor families (Chen et al. 1990, J. Biol: Chem., 265: 3116-3123). This consensus motif is followed by the sequence TYAXPXXXPG (SEQ ID NO:6), which is repeated downstream in MCK-10 in the juxtamembrane domain at positions 585-595. Recently it has been shown that this motif is deleted in the cytoplasmic juxtamembrane region of the activin receptor, serine/threonine kinase, resulting in reduced ligand binding affinity (Attisano et al. 1992, Cell, 68: 97-108).

Please replace the paragraph at page 47, lines 25-34 with the following:

The precursor and the .beta.-subunit of MCK-10 showed strong tyrosine phosphorylation after orthovanadate treatment, (FIG. 6A, left panel) ~~(FIG. 4A, left panel)~~. Surprisingly, the MCK-10-1, containing the 37 amino acid insertion, exhibited lower kinase activity than MCK-10-2. Reprobing the same blot with a peptide antibody raised against the MCK-10 C-terminus revealed equal amounts of expressed receptor and a slight shift of MCK-10-1 precursor and .beta.-subunit due to the additional 37 amino acids of the insertion (FIG. 6A, right panel) ~~(FIG. 4A, right panel)~~.

Please replace the paragraph at page 48, lines 1-15 with the following:

We further analyzed the N-linked glycosylation of the splice variants. Transfected cells were treated overnight with tunicamycin, which inhibits the maturation of proteins by glycosylation. Two affinity purified antibodies raised against peptide sequence of MCK-10 N- and C-terminus, respectively, were used for subsequent immunoprecipitations. Both

antibodies precipitated the predicted 101 kD or 97 kD polypeptides from tunicamycin-treated cells (FIG. 6B) ~~(FIG. 4B)~~. Interestingly, the size of the fully glycosylated forms of MCK-10-1 and MCK-10-2 suggested that the latter was more extensively glycosylated than the putative alternative splice form. This data indicates that the 37 amino acid insertion of MCK-10-1 influences its posttranslational modification which may influence ligand.